Figure 1A
Neutrokine-α

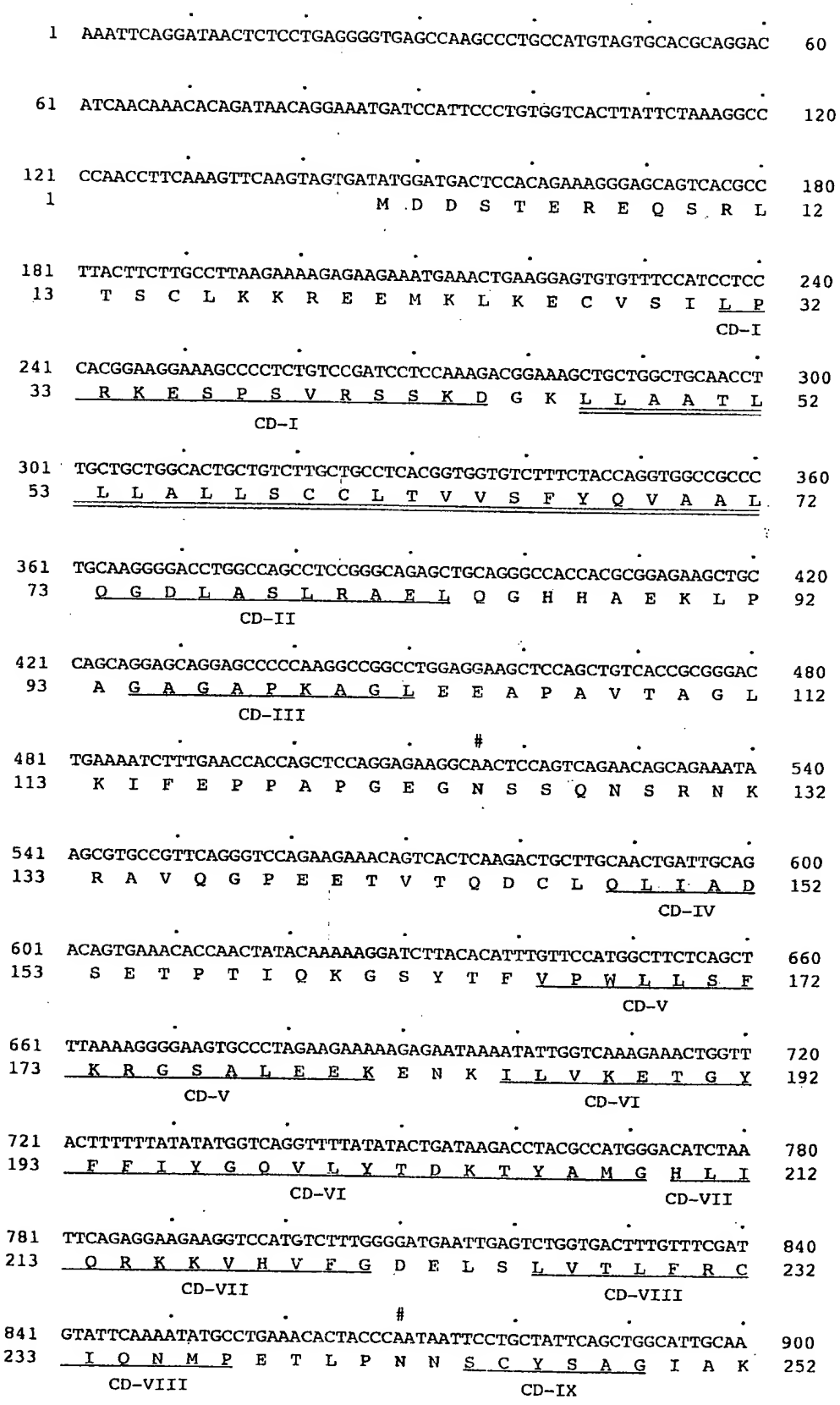


Figure 1B
Neutrokine-α

```
901  AACTGGAAGAAGGAGATGAACTCCAACTTGCAATACCAAGAGAAAATGCACAAATATCAC   960
253    L  E  E  G  D  E  L  Q  L  A  I  P  R  E  N  A  Q  I  S  L   272
                          CD-X

961  TGGATGGAGATGTCACATTTTTTGGTGCATTGAAACTGCTGTGACCTACTTACACCATGT   1020
273    D  G  D  V  T  F  F  G  A  L  K  L  L                       285
                          CD-XI

1021 CTGTAGCTATTTTCCTCCCTTTCTCTGTACCTCTAAGAAGAAAGAATCTAACTGAAAATA   1080

1081 CCAAAAAAAAAAAAAAAAAA  1100
```

FIGURE 2A

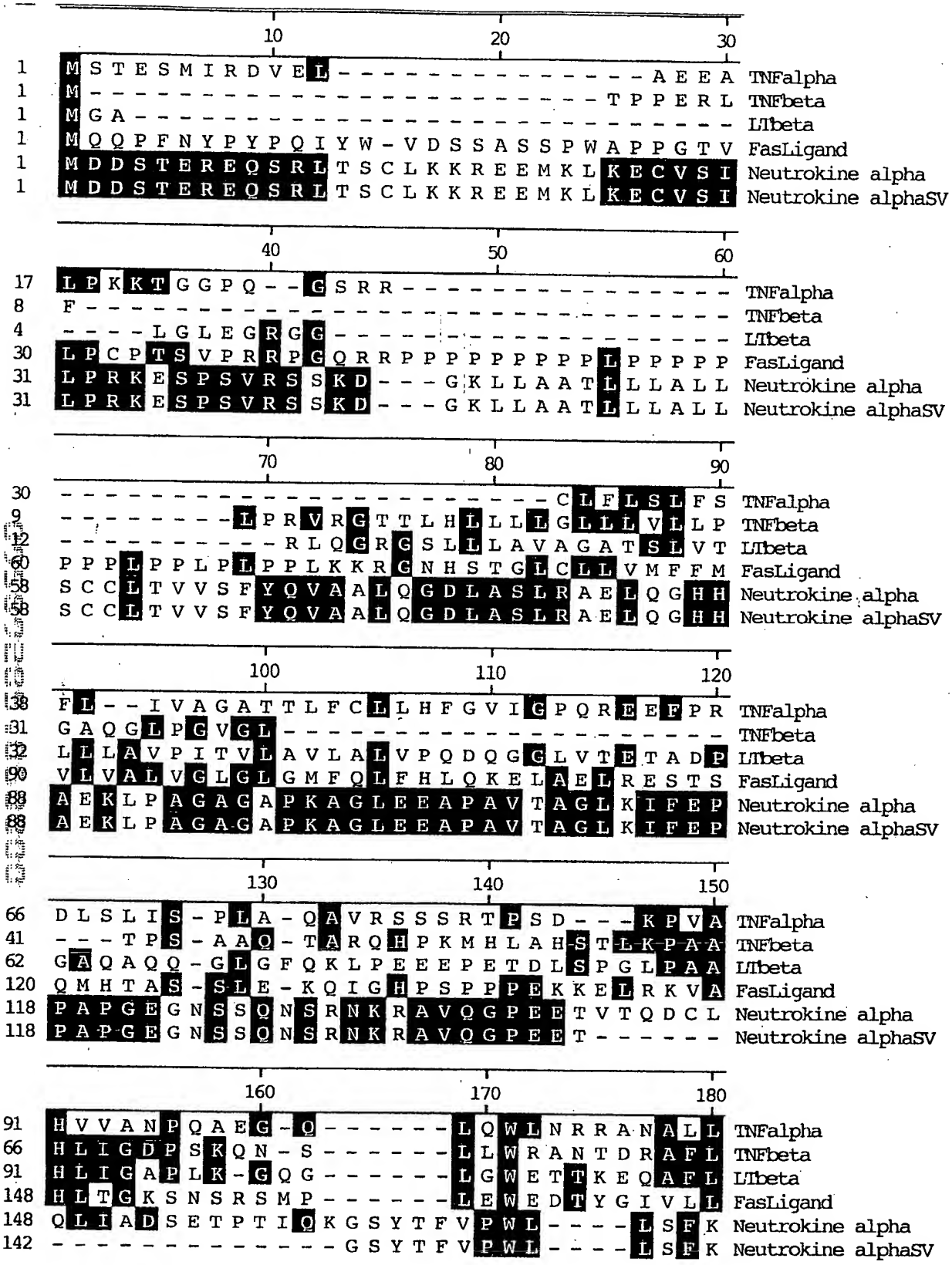

10 20 30
1 MSTESMIRDVEL----------AEEA TNFalpha
1 M----------TPPERL TNFbeta
1 MGA---------- LTbeta
1 MQQPFNYPYPQIYW-VDSSASSPWAPPGTV FasLigand
1 MDDSTEREQSRLTSCLKKREEMKLKECVSI Neutrokine alpha
1 MDDSTEREQSRLTSCLKKREEMKLKECVSI Neutrokine alphaSV
40 50 60
17 LPKKTGGPQ--GSRR---------- TNFalpha
8 F---------- TNFbeta
4 ----LGLEGRGG---------- LTbeta
30 LPCPTSVPRRPGQRRPPPPPPPPPLPPPPP FasLigand
31 LPRKESPSVRSSKD---GKLLAATLLLALL Neutrokine alpha
31 LPRKESPSVRSSKD---GKLLAATLLLALL Neutrokine alphaSV
70 80 90
30 ----------CLFLSLFS TNFalpha
9 ---------LPRVRGTTLHLLLLGLLLVLLP TNFbeta
12 ----------RLQGRGSLLLAVAGATSLVT LTbeta
60 PPPLPPLPLPPLKKRGNHSTGLCLLVMFFM FasLigand
58 SCCLTVVSFYQVAALQGDLASLRAELQGHH Neutrokine alpha
58 SCCLTVVSFYQVAALQGDLASLRAELQGHH Neutrokine alphaSV
100 110 120
38 FL--IVAGATTLFCLLHFGVIGPQREEFPR TNFalpha
31 GAQGLPGVGL---------- TNFbeta
32 LLLAVPITVLAVLALVPQDQGGLVTETADP LTbeta
90 VLVALVGLGLGMFQLFHLQKELAELRESTS FasLigand
88 AEKLPAGAGAPKAGLEEAPAVTAGLKIFEP Neutrokine alpha
88 AEKLPAGAGAPKAGLEEAPAVTAGLKIFEP Neutrokine alphaSV
130 140 150
66 DLSLIS-PLA-QAVRSSSRTPSD---KPVA TNFalpha
41 ---TPS-AAQ-TARQHPKMHLAHSTLKPAA TNFbeta
62 GAQAQQ-GLGFQKLPEEEPETDLSPGLPAA LTbeta
120 QMHTAS-SLE-KQIGHPSPPPEKKELRKVA FasLigand
118 PAPGEGNSSQNSRNKRAVQGPEETVTQDCL Neutrokine alpha
118 PAPGEGNSSQNSRNKRAVQGPEET------- Neutrokine alphaSV
160 170 180
91 HVVANPQAEG-Q------LQWLNRRANALL TNFalpha
66 HLIGDPSKQN-S------LLWRANTDRAFL TNFbeta
91 HLIGAPLK-GQG------LGWETTKEQAFL LTbeta
148 HLTGKSNSRSMP------LEWEDTYGIVLL FasLigand
148 QLIADSETPTIQKGSYTFVPWL----LSFK Neutrokine alpha
142 ----------GSYTFVPWL----LSFK Neutrokine alphaSV

FIGURE 2B

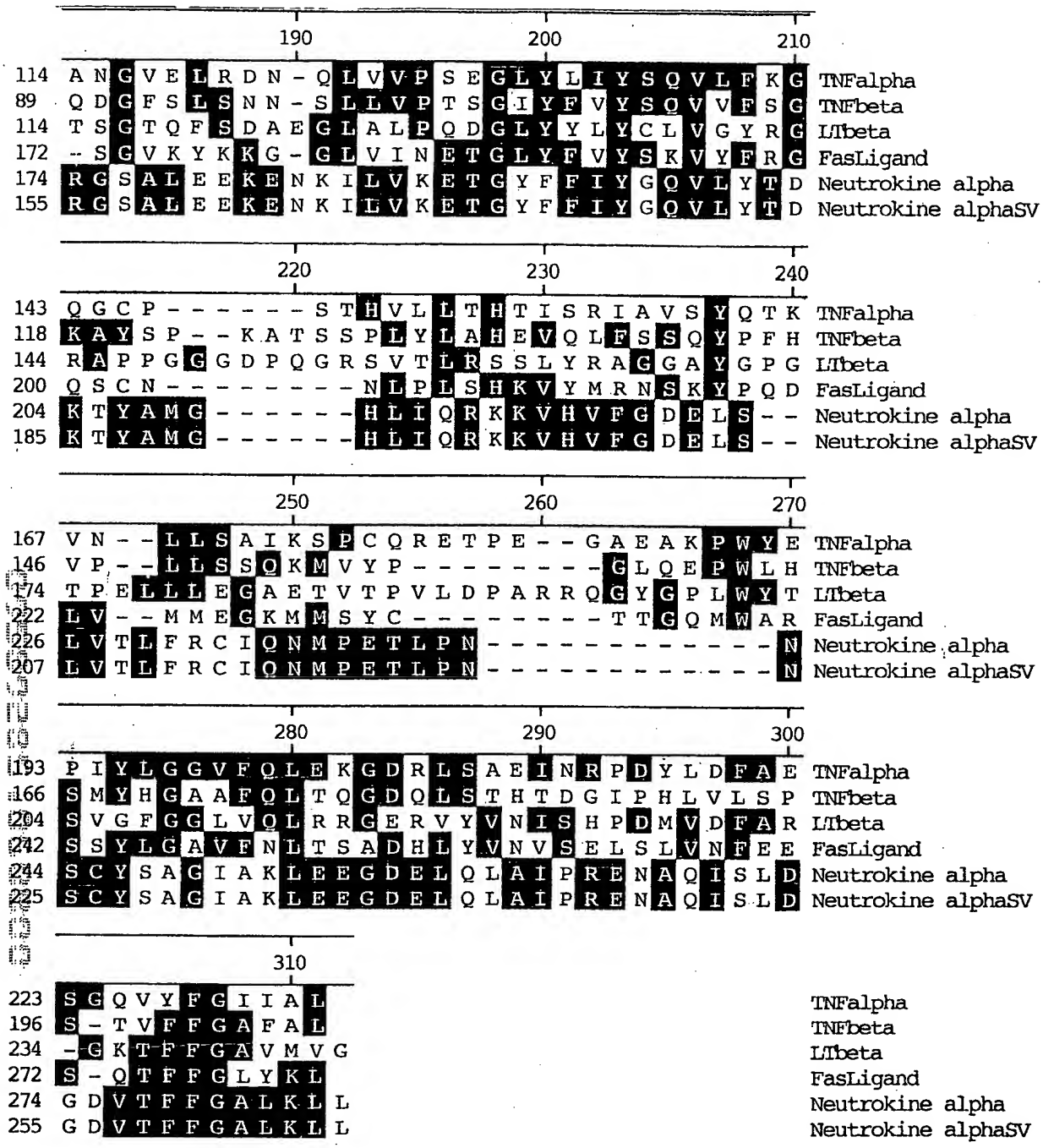

190 200 210
114 ANGVELRDN-QLVVPSEGLYLIYSQVLFKG TNFalpha
89 QDGFSLSNN-SLLVPTSGIYFVYSQVVFSG TNFbeta
114 TSGTQFSDAEGLALPQDGLYYLYCLVGYRG LTbeta
172 --SGVKYKKG-GLVINETGLYFVYSKVYFRG FasLigand
174 RGSALEEKENKILVKETGYFFIYGQVLYTD Neutrokine alpha
155 RGSALEEKENKILVKETGYFFIYGQVLYTD Neutrokine alphaSV
220 230 240
143 QGCP-------STHVLLTHTISRIAVSYQTK TNFalpha
118 KAYSP--KATSSPLYLAHEVQLFSSQYPFH TNFbeta
144 RAPPGGGDPQGRSVTLRSSLYRAGGAYGPG LTbeta
200 QSCN---------NLPLSHKVYMRNSKYPQD FasLigand
204 KTYAMG-------HLIQRKKVHVFGDELS-- Neutrokine alpha
185 KTYAMG-------HLIQRKKVHVFGDELS-- Neutrokine alphaSV
250 260 270
167 VN--LLSAIKSPCQRETPE--GAEAKPWYE TNFalpha
146 VP--LLSSQKMVYP---------GLQEPWLH TNFbeta
174 TPELLLEGAETVTPVLDPARRQGYGPLWYT LTbeta
222 LV--MMEGKMMSYC---------TTGQMWAR FasLigand
226 LVTLFRCIQNMPETLPN----------------N Neutrokine alpha
207 LVTLFRCIQNMPETLPN----------------N Neutrokine alphaSV
280 290 300
193 PIYLGGVFQLEKGDRLSAEINRPDYLDFAE TNFalpha
166 SMYHGAAFQLTQGDQLSTHTDGIPHLVLSP TNFbeta
204 SVGFGGLVQLRRGERVYVNISHPDMVDFAR LTbeta
242 SSYLGAVFNLTSADHLYVNVSELSLVNFEE FasLigand
244 SCYSAGIAKLEEGDELQLAIPRENAQISLD Neutrokine alpha
225 SCYSAGIAKLEEGDELQLAIPRENAQISLD Neutrokine alphaSV
310
223 SGQVYFGIIAL TNFalpha
196 S-TVFFGAFAL TNFbeta
234 -GKTFFGAVMVG LTbeta
272 S-QTFFGLYKL FasLigand
274 GDVTFFGALKLL Neutrokine alpha
255 GDVTFFGALKLL Neutrokine alphaSV

Figure 3
Neutrokine-α

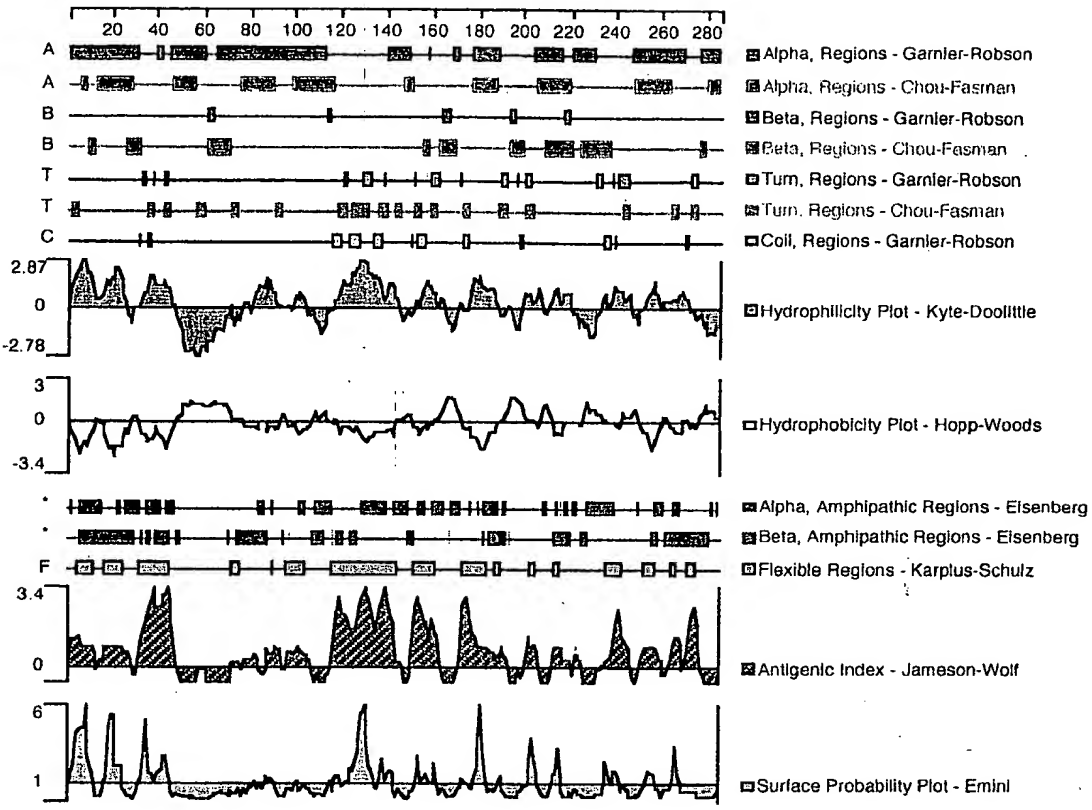


FIGURE 4 A

```
          1                                                   50
HSOAD55R  .........A GGNTAACTCT CCTGAGGGGT GAGCCAAGCC CTGCCATGTA
HNEDU15X  ...AAATTCA GGATAACTCT CCTGAGGGGT GAGCCAAGCC CTGCCATGTA
HSLAH84R  .AATTCGGCA NAGNAAACTG GTTACTTTTT TATATATGGT CAGGTTTTAT
HLTBM08R  AATTCGGCAC GAGCAAGGCC GGCCTGGAGG AAGCTCCAGC TGTCACCGCG

          51                                                  100
HSOAD55R  GTGCACGCAG GACATCANCA A..ACACANN NNNCAGGAAA TAATCCATTC
HNEDU15X  GTGCACGCAG GACATCAACA A..ACACAGA TAACAGGAAA TGATCCATTC
HSLAH84R  ATACTGATAA GACCTACGCC ATGGGACATC TAGTTCAGAG GAAGAAGGTC
HLTBM08R  GGACTGAAAA TCTTTGAACC ACCAGCTCCA GGAGAAGGCA ACTCCAGTCA

          101                                                 150
HSOAD55R  CCTGTGGTCA CTTATTCTAA AGGCCCCAAC CTTCAAAGTT CAAGTAGTGA
HNEDU15X  CCTGTGGTCA CTTATTCTAA AGGCCCCAAC CTTCAAAGTT CAAGTAGTGA
HSLAH84R  CATGTCTTTG GGGATGAATT GAGTCTGGTG ACTTTGTTTC GATGTATTCA
HLTBM08R  GAACAGCAGA AATAAGCGTG CCGTTCAGGG TCCAGAAGAA ACAGTCACTC

          151                                                 200
HSOAD55R  TATGGATGAC TCCACAGAAA GGGAGCAGTC ACGCCTTACT TCTTGCCTTA
HNEDU15X  TATGGATGAC TCCACAGAAA GGGAGCAGTC ACGCCTTACT TCTTGCCTTA
HSLAH84R  AAATATGCCT GAAACACTAC CCAATAATTC CTGCTATTCA GCTGGCATTG
HLTBM08R  AAGACTGCTT GCAACTGNTT GCAGACAGTG AAACACCAAC TATACAAAAA

          201                                                 250
HSOAD55R  AGAAAAGAGA AGAAATGAAA CTGNAAGGAG TGTGTTTCCA TCCTCCCACG
HNEDU15X  AGAAAAGAGA AGAAATGAAA CT.GAAGGAG TGTGTTTCCA TCCTCCCACG
HSLAH84R  CAAAACTGGN AGGAAGGA.. ...GATGAAC TCCAACTTGC AATACCAGGG
HLTBM08R  GGCTCCCTTC TGNTGCCACA TTTGGGCCAA GGAATGGAGA GATTTCTTCG

          251                                                 300
HSOAD55R  GAAGGAAAGC CCCTCTNTCC GATCCTCCAA AGACGGAAAG CTGCTGGCTG
HNEDU15X  GAAGGAAAGC CCCTCTGTCC GATCCTCCAA AGACGGAAAG CTGCTGGCTG
HSLAH84R  GAAAATGCAC AATTATCACT GGGATGGAGA TGTTCACATT TTTTGGGTGC
HLTBM08R  TCTGGAAACA TTTTGCCAAA CTCTTCAGAT ACTCTTTNCT CTCTGGGAAT

          301                                                 350
HSOAD55R  CAACCTTGNT GNTGGCATTG TGTTCTTGCT GNCTCAAGGT GGTGTTNTT.
HNEDU15X  CAACCTTGCT GCTGGCACTG CTGTCTTGCT GCCTCACGGT GGTGTCTTTC
HSLAH84R  CATTGAAACT GCTGTGACCT NCTTACANCA NGTGCTGTTN GCTATTTTNC
HLTBM08R  CAAAGGAAAA TCTCTACTTA GATTNACACA TTTGTTCCCA TGGGTNTCTT

          351                                                 400
HSOAD55R  .......... .......... .......... .......... ..........
HNEDU15X  TACCAGGTGG CCGCCCTGCA AGGGGACCTG GCCAGCCTCC GGGCAGAGCT
HSLAH84R  CTNCCTNTTC TNTGGTAACC TCTTAGGAAG GAAGGATTCT TAACTGGGAA
HLTBM08R  AAGTTTTAAA AGGGGAGTGC CCTTAGGAGG AAAAGGGGAT AAATATTGGC
```

FIGURE 4B

```
           401                                                  450
HSOAD55R   .......... .......... .......... .......... ..........
HNEDU15X   GCAGGGCCAC CACGCGGAGA AGCTGCCAGC AGGAGCAGGA GCCCCCAAGG
HSLAH84R   ATAACCCAAA AAAANNTTAA ANGGGTANGN GNNANANGNG GGGNNGTTNN
HLTBM08R   CAAGGNACTG GTTANTTTNT AAATATGGTC AGGTTTNTAT ANCTGGTAGG

           451                                                  500
HSOAD55R   .......... .......... .......... .......... ..........
HNEDU15X   CCGGCCTGGA GGAAGCTCCA GCTGTCACCG CGGGACTGAA AATCTTTGAA
HSLAH84R   CNNGNNGNNT TTTNGGNNTA TNTTNTNNTN GGGNNNNGTA AAAATGGGGC
HLTBM08R   CCTCGCCATG GGCATTNATT CANGGNGAGG NCNNTCTTTT GGGNTGA...

           501                                                  550
HSOAD55R   .......... .......... .......... .......... ..........
HNEDU15X   CCACCAGCTC CAGGAGAAGG CAACTCCAGT CAGAACAGCA GAAATAAGCG
HSLAH84R   CNANGGGGGN TTTTT..... .......... .......... ..........
HLTBM08R   .......... .......... .......... .......... ..........

           551                                                  600
HSOAD55R   .......... .......... .......... .......... ..........
HNEDU15X   TGCCGTTCAG GGTCCAGAAG AAACAGTCAC TCAAGACTGC TTGCAACTGA
HSLAH84R   .......... .......... .......... .......... ..........
HLTBM08R   .......... .......... .......... .......... ..........

           601                                                  650
HSOAD55R   .......... .......... .......... .......... ..........
HNEDU15X   TTGCAGACAG TGAAACACCA ACTATACAAA AAGGATCTTA CACATTTGTT
HSLAH84R   .......... .......... .......... .......... ..........
HLTBM08R   .......... .......... .......... .......... ..........

           651                                                  700
HSOAD55R   .......... .......... .......... .......... ..........
HNEDU15X   CCATGGCTTC TCAGCTTTAA AAGGGGAAGT GCCCTAGAAG AAAAAGAGAA
HSLAH84R   .......... .......... .......... .......... ..........
HLTBM08R   .......... .......... .......... .......... ..........

           701                                                  750
HSOAD55R   .......... .......... .......... .......... ..........
HNEDU15X   TAAAATATTG GTCAAAGAAA CTGGTTACTT TTTTATATAT GGTCAGGTTT
HSLAH84R   .......... .......... .......... .......... ..........
HLTBM08R   .......... .......... .......... .......... ..........

           751                                                  800
HSOAD55R   .......... .......... .......... .......... ..........
HNEDU15X   TATATACTGA TAAGACCTAC GCCATGGGAC ATCTAATTCA GAGGAAGAAG
HSLAH84R   .......... .......... .......... .......... ..........
HLTBM08R   .......... .......... .......... .......... ..........
```

FIGURE 4C

```
            801                                                       850
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    GTCCATGTCT TTGGGGATGA ATTGAGTCTG GTGACTTTGT TTCGATGTAT
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            851                                                       900
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    TCAAAATATG CCTGAAACAC TACCCAATAA TTCCTGCTAT TCAGCTGGCA
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            901                                                       950
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    TTGCAAAACT GGAAGAAGGA GATGAACTCC AACTTGCAAT ACCAAGAGAA
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            951                                                      1000
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    AATGCACAAA TATCACTGGA TGGAGATGTC ACATTTTTTG GTGCATTGAA
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            1001                                                     1050
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    ACTGCTGTGA CCTACTTACA CCATGTCTGT AGCTATTTTC CTCCCTTTCT
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            1051                                                     1100
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    CTGTACCTCT AAGAAGAAAG AATCTAACTG AAAATACCAA AAAAAAAAAA
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            1101
HSOAD55R    ......
HNEDU15X    AAAAAA
HSLAH84R    ......
HLTBM08R    ......
```

Figure 5A
Neutrokine-αSV

```
   1  ATGGATGACTCCACAGAAAGGGAGCAGTCACGCCTTACTTCTTGCCTTAAGAAAAGAGAA   60
   1  M  D  D  S  T  E  R  E  Q  S  R  L  T  S  C  L  K  K  R  E    20

  61  GAAATGAAACTGAAGGAGTGTGTTTCCATCCTCCCACGGAAGGAAAGCCCCTCTGTCCGA  120
  21  E  M  K  L  K  E  C  V  S  I  L  P  R  K  E  S  P  S  V  R    40
                                                 CD-I

 121  TCCTCCAAAGACGGAAAGCTGCTGGCTGCAACCTTGCTGCTGGCACTGCTGTCTTGCTGC  180
  41  S  S  K  D  G  K  L  L  A  A  T  L  L  L  A  L  L  S  C  C    60
         CD-I

 181  CTCACGGTGGTGTCTTTCTACCAGGTGGCCGCCCTGCAAGGGGACCTGGCCAGCCTCCGG  240
  61  L  T  V  V  S  F  Y  Q  V  A  A  L  Q  G  D  L  A  S  L  R    80
                                                 CD-II

 241  GCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGCCAGCAGGAGCAGGAGCCCCCAAGGCC  300
  81  A  E  L  Q  G  H  H  A  E  K  L  P  A  G  A  G  A  P  K  A   100
         CD-II                                   CD-III

 301  GGCCTGGAGGAAGCTCCAGCTGTCACCGCGGGACTGAAAATCTTTGAACCACCAGCTCCA  360
 101  G  L  E  E  A  P  A  V  T  A  G  L  K  I  F  E  P  P  A  P   120
      CD-III
               #
 361  GGAGAAGGCAACTCCAGTCAGAACAGCAGAAATAAGCGTGCCGTTCAGGGTCCAGAAGAA  420
 121  G  E  G  N  S  S  Q  N  S  R  N  K  R  A  V  Q  G  P  E  E   140

 421  ACAGGATCTTACACATTTGTTCCATGGCTTCTCAGCTTTAAAAGGGGAAGTGCCCTAGAA  480
 141  T  G  S  Y  T  F  V  P  W  L  L  S  F  K  R  G  S  A  L  E   160
                                                 CD-IV

 481  GAAAAAGAGAATAAAATATTGGTCAAAGAAACTGGTTACTTTTTTATATATGGTCAGGTT  540
 161  E  K  E  N  K  I  L  V  K  E  T  G  Y  F  F  I  Y  G  Q  V   180
         CD-IV                                CD-V

 541  TTATATACTGATAAGACCTACGCCATGGGACATCTAATTCAGAGGAAGAAGGTCCATGTC  600
 181  L  Y  T  D  K  T  Y  A  M  G  H  L  I  Q  R  K  K  V  H  V   200
                  CD-VI                  CD-VII

 601  TTTGGGGATGAATTGAGTCTGGTGACTTTGTTTCGATGTATTCAAAATATGCCTGAAACA  660
 201  F  G  D  E  L  S  L  V  T  L  F  R  C  I  Q  N  M  P  E  T   220
      CD-VIII                  CD-VIII
            #
 661  CTACCCAATAATTCCTGCTATTCAGCTGGCATTGCAAAACTGGAAGAAGGAGATGAACTC  720
 221  L  P  N  N  S  C  Y  S  A  G  I  A  K  L  E  E  G  D  E  L   240
                     CD-IX                        CD-X

 721  CAACTTGCAATACCAAGAGAAAATGCACAAATATCACTGGATGGAGATGTCACATTTTTT  780
 241  Q  L  A  I  P  R  E  N  A  Q  I  S  L  D  G  D  V  T  F  F   260
            CD-X                                          CD-XI

 781  GGTGCATTGAAACTGCTGTGACCTACTTACACCATGTCTGTAGCTATTTTCCTCCCTTTC  840
 261  G  A  L  K  L  L                                             266
         CD-XI
```

Figure 5B
Neutrokine-αSV

841 TCTGTACCTCTAAGAAGAAAGAATCTAACTGAAAATACCAAAAAAAAAAAAAAAAAAAAA 900

901 AAA 903

Figure 6
Neutrokine-αSV

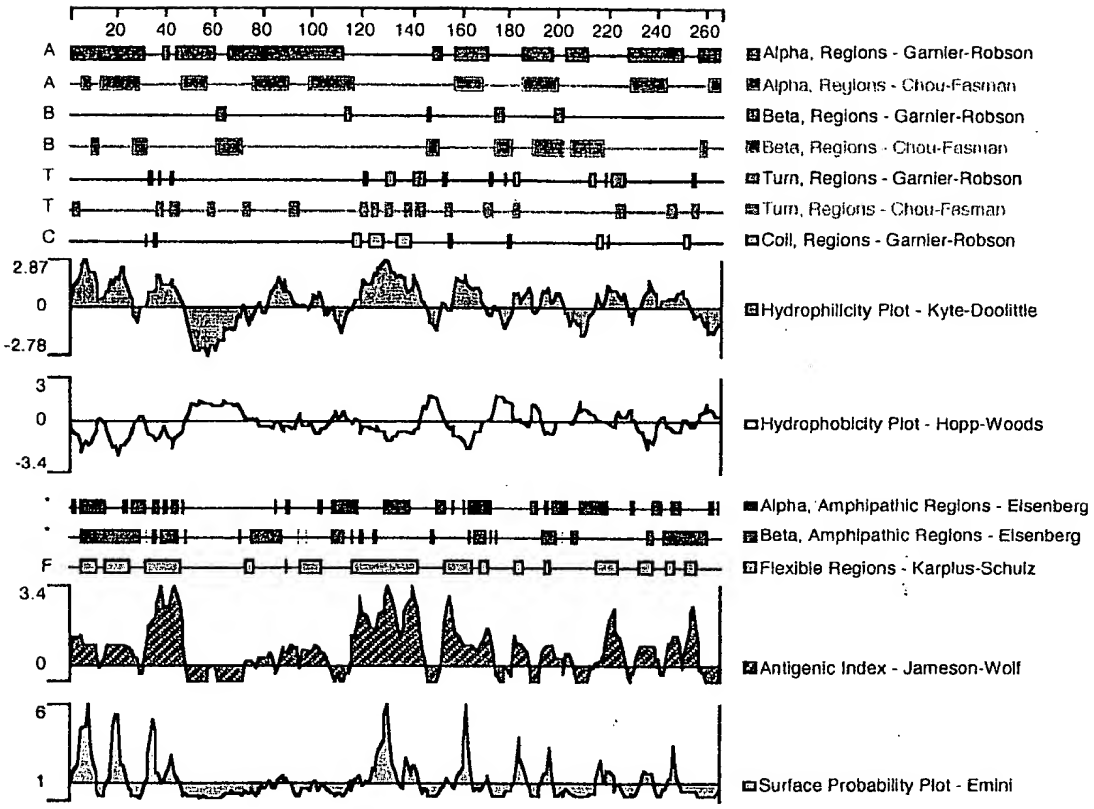
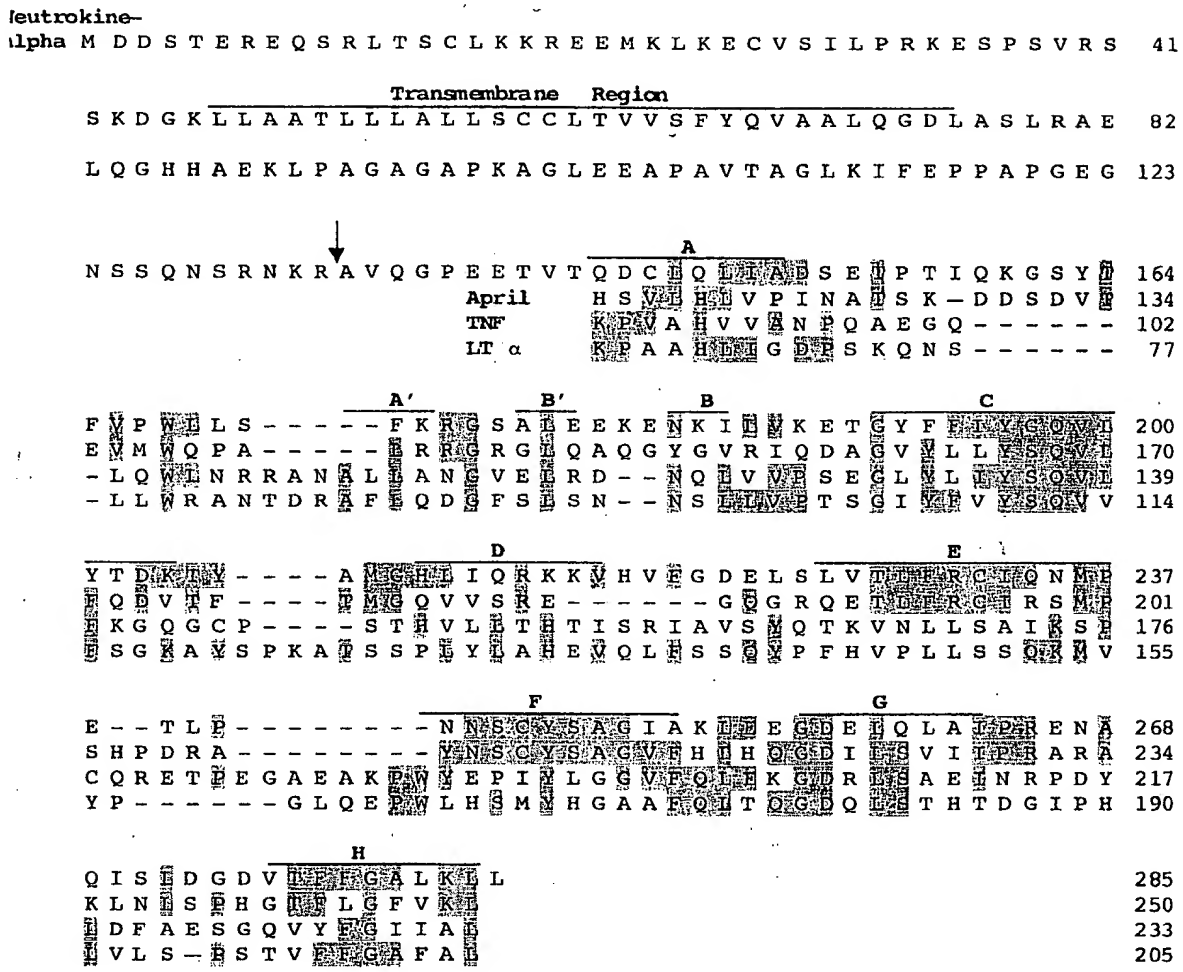


Figure 7

a.


leutrokine-
ılpha M D D S T E R E Q S R L T S C L K K R E E M K L K E C V S I L P R K E S P S V R S 41
Transmembrane Region
S K D G K L L A A T L L L A L L S C C L T V V S F Y Q V A A L Q G D L A S L R A E 82
L Q G H H A E K L P A G A G A P K A G L E E A P A V T A G L K I F E P P A P G E G 123
A
N S S Q N S R N K R A V Q G P E E T V T Q D C L Q L I A D S E T P T I Q K G S Y T 164
April H S V L H L V P I N A T S K – D D S D V T 134
TNF K P V A H V V A N P Q A E G Q – – – – – – – 102
LT α K P A A H L I G D P S K Q N S – – – – – – – 77
A′ B′ B C
F V P W L L S – – – – – F K R G S A L E E K E N K I L V K E T G Y F F I Y G Q V L 200
E V M W Q P A – – – – – E R R G R G Q A Q G Y G V R I Q D A G V Y L L Y S Q V L 170
– L Q W L N R R A N A L L A N G V E L R D – – N Q L V V P S E G L Y L I Y S Q V L 139
– L L W R A N T D R A F L Q D G F S L S N – – N S L L V T S G I Y F V Y S Q V V 114
D E
Y T D K T Y – – – – A M G H F I Q R K K V H V F G D E L S L V T F F R C I Q N M P 237
F Q E V F F – – – – E M G Q V V S R E – – – – – – G Q G R Q E T L F R G I R S M P 201
E K G Q G C P – – – – S T H V L T T I S R I A V S Y Q T K V N L L S A I K S P 176
E S G K A K S P K A E S S P L Y L A H E V Q L H S S Q K P F H V P L L S S Q K M V 155
F G
E – – T L P – – – – – – – – – N N S C V S A G I A K L M E E G D E L Q L A I P R E N A 268
S H P D R A – – – – – – – – – Y N S C Y S A G V F H L H Q G D I L S V I I P R A R A 234
C Q R E T L E G A E A K P W Y E P I Y L G G V F Q L E K G D R L S A E I N R P D Y 217
Y P – – – – – – – G L Q E P W L H S M Y H G A A F Q L T Q G D Q L S T H T D G I P H 190
H
Q I S E D G D V L P F G A L K L L 285
K L N S P H G L F L G F V K L 250
E D F A E S G Q V Y F G I I A E 233
E V L S – P S T V F F G A F A E 205

b.

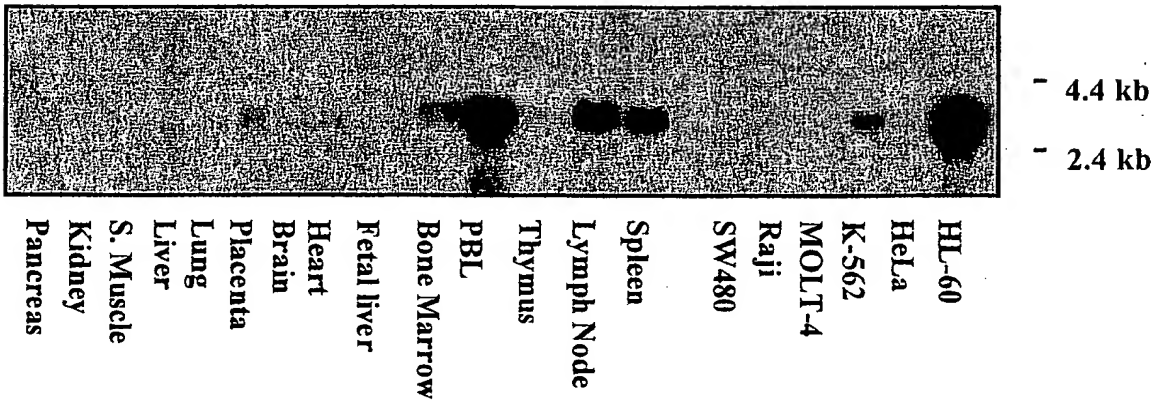
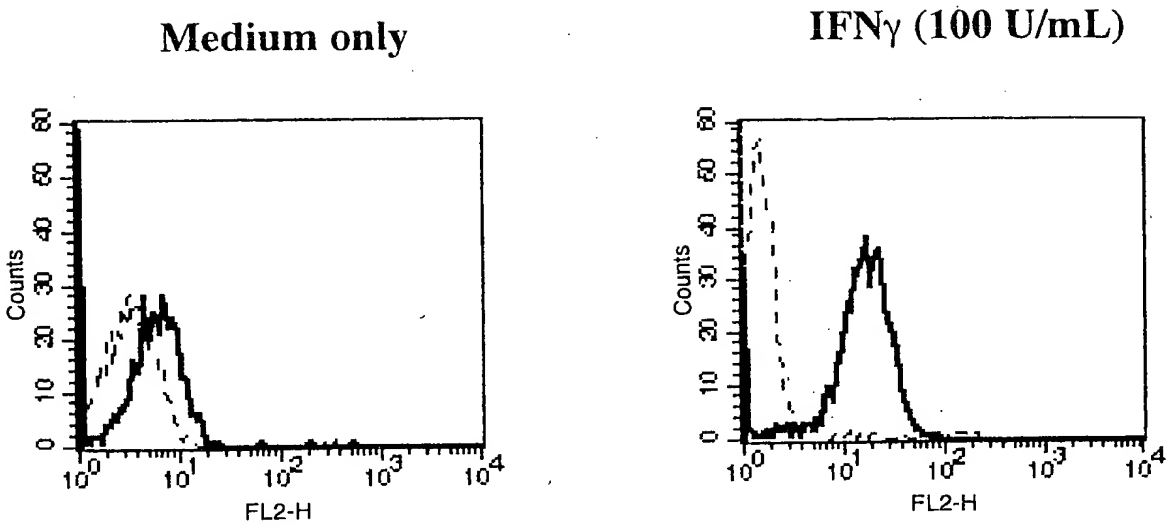

4.4 kb
2.4 kb
Pancreas
Kidney
S. Muscle
Liver
Lung
Placenta
Brain
Heart
Fetal liver
Bone Marrow
PBL
Thymus
Lymph Node
Spleen
SW480
Raji
MOLT-4
K-562
HeLa
HL-60

Figure 8

a.


Medium only
IFNγ (100 U/mL)
Counts
FL2-H

b.

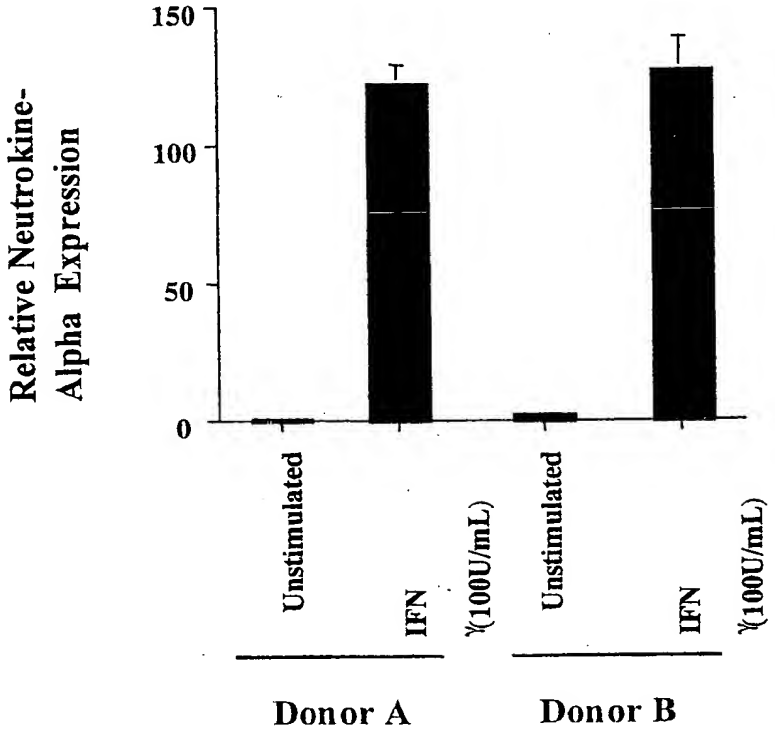
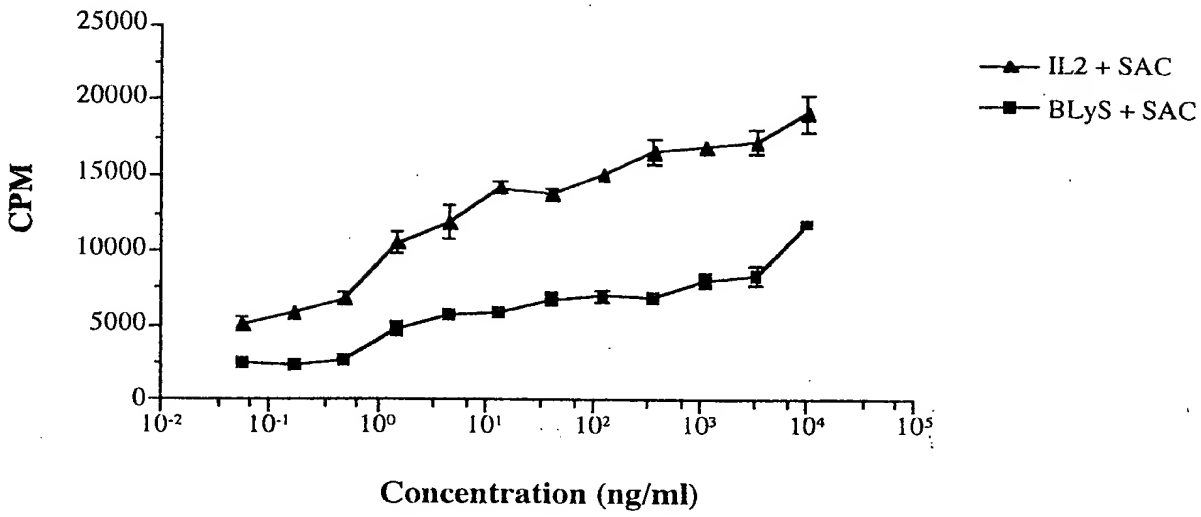

Relative Neutrokine-Alpha Expression
150
100
50
0
Unstimulated
IFNγ (100U/mL)
Unstimulated
IFNγ (100U/mL)
Donor A
Donor B

Figure 9

a.


25000
20000
15000
10000
5000
0
CPM
10^{-2}
10^{-1}
10^{0}
10^{1}
10^{2}
10^{3}
10^{4}
10^{5}
Concentration (ng/ml)
IL2 + SAC
BLyS + SAC

b.

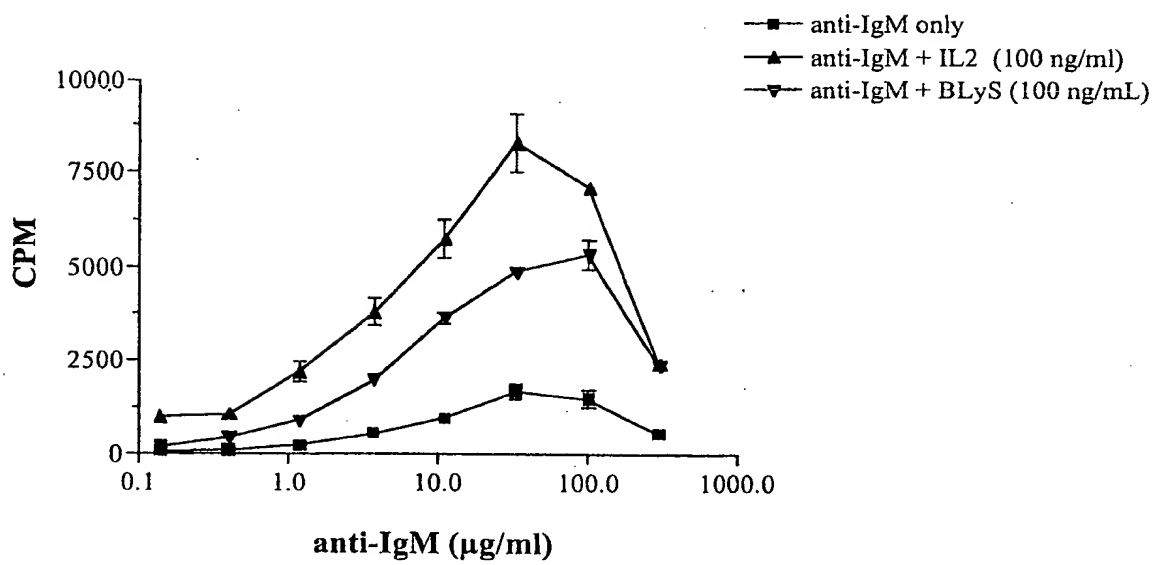
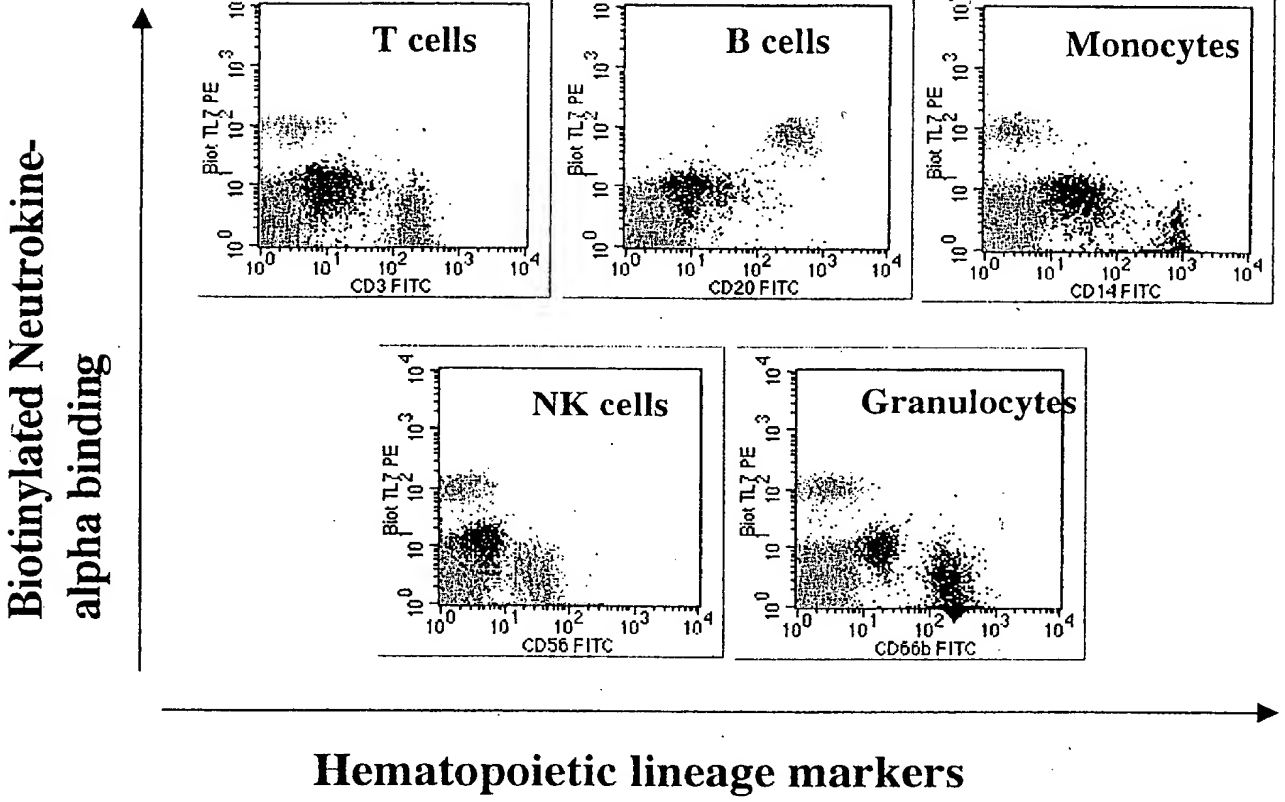

10000
7500
5000
2500
0
CPM
0.1
1.0
10.0
100.0
1000.0
anti-IgM (µg/ml)
anti-IgM only
anti-IgM + IL2 (100 ng/ml)
anti-IgM + BLyS (100 ng/mL)

Figure 10

a.


Biotinylated Neutrokine-alpha binding
T cells
B cells
Monocytes
NK cells
Granulocytes
Biot TL7 PE
CD3 FITC
CD20 FITC
CD14 FITC
CD56 FITC
CD66b FITC
Hematopoietic lineage markers

b.

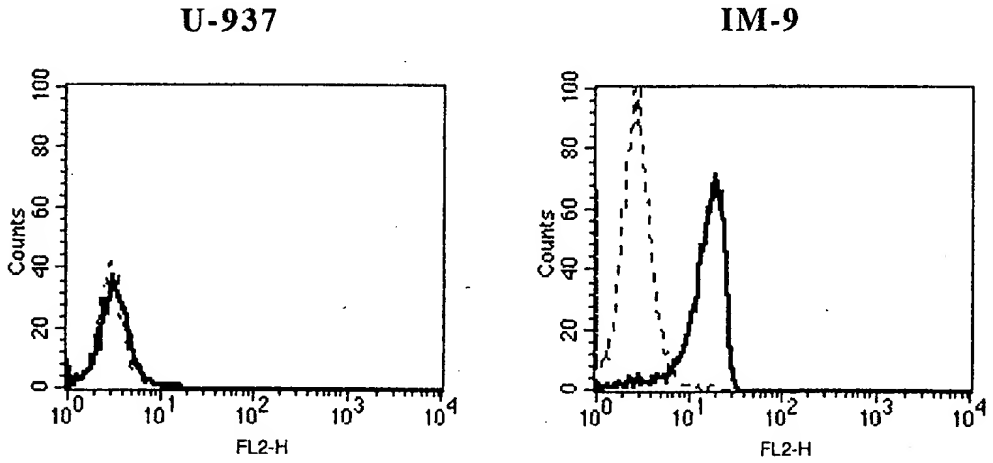
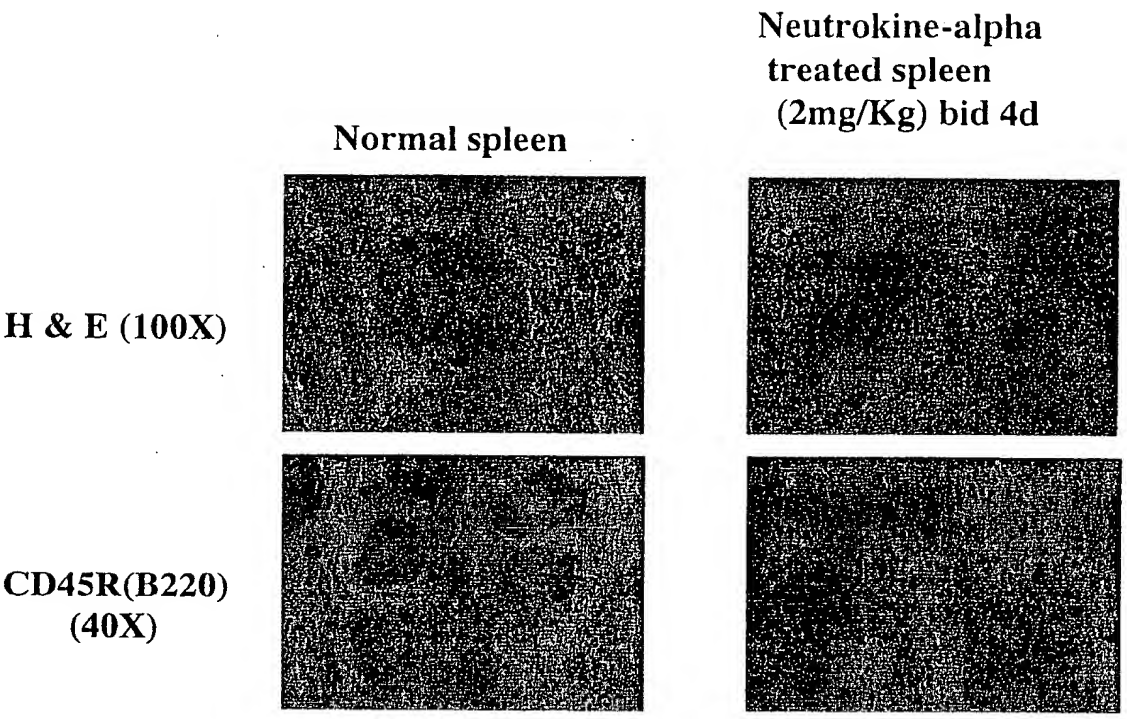
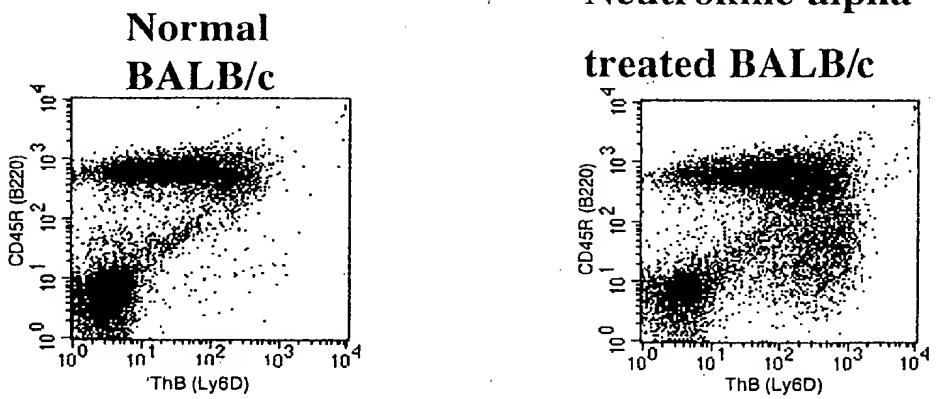

U-937
IM-9
Counts
FL2-H

Figure 11

a.



b.



c.